Molecular characterization of *Secoviridae* and *Potexvirus* infecting yams (*Dioscorea spp*)

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The prevalence of virus species is generally high among vegetatively-propagated crops, because they cannot be sanitized via seed production and therefore accumulate viruses over long periods of time. In yams (*Dioscorea* spp), viruses belonging to the families *Alphaflexiviridae* (genus potexvirus), *Betaflexiviridae* (genus carlavirus), *Caulimoviridae* (genus badnavirus), *Cucumoviridae* (genus cucumovirus) and *Potyviridae* (genera macluravirus and potyvirus) have been characterized so far. However, it is likely that the diversity of viral species infecting this crop remains underestimated. To test this hypothesis, *in silico* analyses of ESTs of *Dioscorea alata* were performed and unveiled the existence of sequences corresponding to several known genera of yam viruses, such as badnavirus and macluravirus, and also to families of unknown yam-associated viruses, including *Geminiviridae* and *Secoviridae*. This result has prompted a search for yet uncharacterized viruses infecting yams.
RT-PCR performed on crude extracts of symptomatic yams (*D. alata*, *D. trifida*) following direct binding of viral particles and using available degenerate primers raised distinct amplification products, which were cloned and sequenced. Some of them displayed significant levels of homologies with potexviruses and with viruses of the family *Secoviridae.* The 3' end of their genomes was successfully amplified by 3' RACE, cloned and sequenced. Sequence analyses and phylogenetic analyses confirmed the existence in yams of new viral species within the genus potexvirus and the family *Secoviridae*. These results highlight the need to improve the current taxonomy of yam potexviruses and suggest to further explore the diversity of viruses of the family *Secoviridae* in yams.

Keywords: Yams; *Dioscoreacae*; *Secoviridae*; *Alphaflexiviridae*; taxonomy